Amendments to the Specification

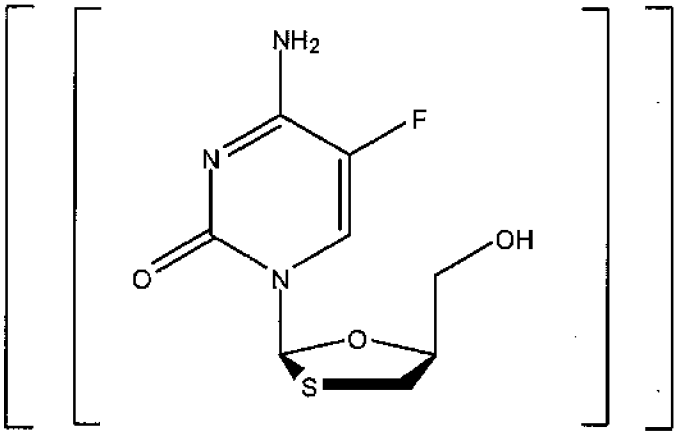
Please note: Paragraph numbers are taken from the application which published as US 2005/0196379. Page and line numbers are from the specification as filed. Please delete paragraph [0013] starting at page 3, line 11 of the specification as filed and replace paragraph [0013] with the following paragraph:

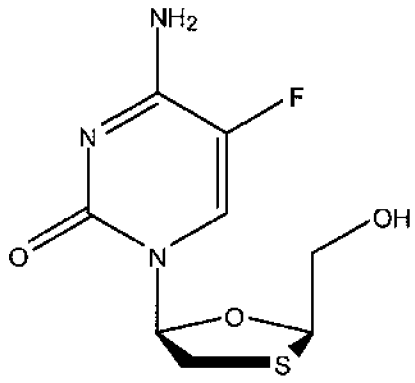
[0013] Although 3TC efficiently inhibits HBV replication, the slow kinetics of viral elimination during 3TC therapy (Nowak, M., S. Bonhoeffer, et al. 1996. *Proc. Natl. Acad. Sci. USA* 93:4398-4402) and the spontaneous viral genome variability lead to the emergence of drug-resistant mutants which carry mutations affecting the reverse transcriptase (RT) domain (Mason, W. S., J. Cullen, et al. 1998. *Virology* 245:18-32. Nafa, S., S. Ahmed, et al. 2000. *Hepatology* 32:1078-1088; Melegari, M., P. P. Scaglioni, and J. R. Wands. 1998 *Hepatology* 27:628-633; Seigneres, B., C. Pichoud, et al. 2000. *J. Infect. Dis.* 181:1221-1233). Approximately 50% of treated patients develop viral resistance after 3 years of treatment with 3TC (Leung, N. W., C. L. Lai, et al. 2001. *Hepatology* 33:1527-1532). Resistance to nucleoside analogs is associated with substitutions in the nucleic acid sequence of the polymerase gene causing changes in the amino acid sequence of the HBV RT, notably in the YMDD (SEQ ID NO: 1) motif within the catalytic site. The most common polymerase variant is the rtL180M-plus-M204V change (according to the recent genotype-independent nomenclature for HBV drug-resistant variants) (Stuyver, L. J., S. A. Locarnini, et al. 2001. *Hepatology* 33:751-757) that associates a mutation in the catalytic site (rtM204V) with a compensatory mutation in the B domain of the RT (rtL180M) which provides a higher replication capacity to the catalytic site variant (Allen, M. I., M. Deslauriers, et al. 1998. *Hepatology* 27:1670-1677. Chayama, K., Y. Suzuki, et al. 1998. *Hepatology* 27:1711-

1716. Melegari, M., P. P. Scaglioni, and J. R. Wands. 1998. *Hepatology* 27:628-633. Ono, S. K., N. Kato, et al. 2001. *J. Clin. Investig.* 107:449-455. Seigneres, B., S. Aguesse-Germon, et al. 2001. J. *Hepatol.* 34:114-122).

Please delete paragraph [0017] starting at page 4, line 15 of the specification as filed and replace paragraph [0017] with the following paragraph:

[0017] β-L-FTC ((β-2-hydroxymethyl-5-(5-fluorocytosin-1-yl)-1,3-oxathiolane, Emtriva; emtricitabine) is approved for the treatment of HIV and currently in human clinical trials for the treatment of hepatitis B virus infection. The compound ~~show~~ shows strong activity against hepatitis B virus in duck models (Aguesse-Germon, S., S.-H, Liu, *et al. Antimicrob. Agents Chemother.* **1998**, *42*, 369-376; Seigneres, B., C. Pichoud, *et al.* **2000**) and woodchucks. In a woodchuck model of HBV, FTC was found to inhibit viral replication but not induce viral clearance. (Cullen, J. M., S. L. Smith, *et al. Antimicrob. Agents Chemother.* **1997**, *41*, 2076-2082; Korba, B. E., R. F. Schinazi, P., *et al. Antimicrob. Agents Chemother.* **2000**, *44*, 1757-60).



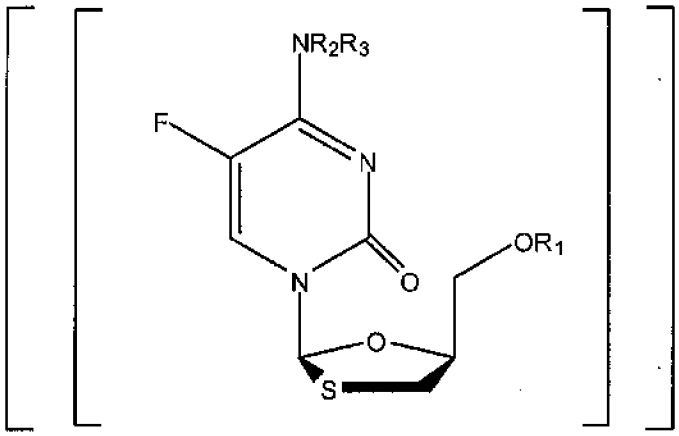


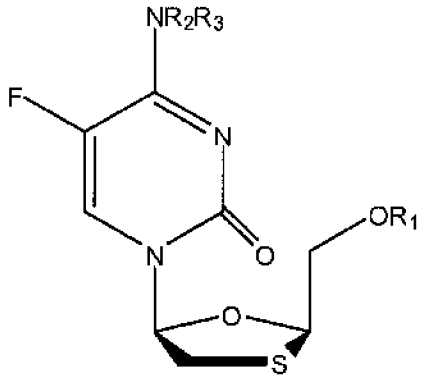
FTC

β-L

Please delete paragraph [0045] starting at page 10, line 17 of the specification as filed and replace paragraph [0045] with the following paragraph:

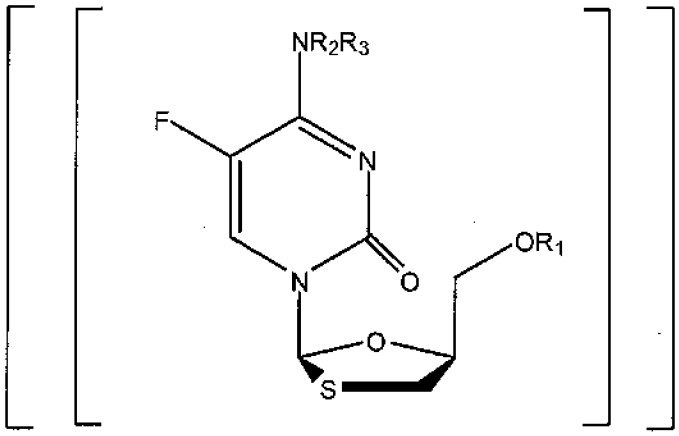
[0045] in combination and/or alternation with a β-L-nucleoside of the formula:

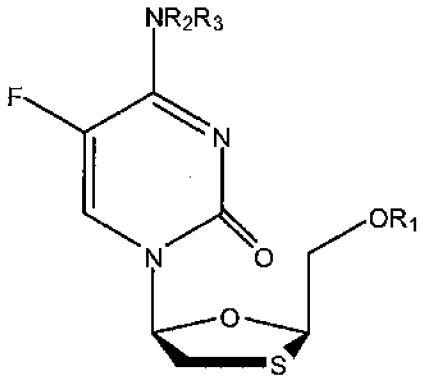




Please delete paragraph [0073] starting at page 16, line 13 of the specification as filed and replace paragraph [0073] with the following paragraph:

[0073] in combination and/or alternation with a β-L-nucleoside of the formula:





Please delete paragraph [0247] starting at page 55, line 19 of the specification as filed and replace paragraph [0247] with the following paragraph:

[0247] WHV DNA was amplified by PCR from serum collected either at the end of the treatment period or at the best point before the animal death. DNA from serum was amplified for 35 cycles (94°C. for 1 min, 50°C. for 1 min, and 72°C. for 1 min) with Taq polymerase and a specific primer pair (5'-AGATTGGTTGGTGCACTTCT-3 (SEQ ID NO: 2) (nucleotides 385 to 403) and 5'-ATTGTCAGTGCCCAACA-3' (SEQ ID NO: 3) (nucleotides 1468 to 1461), corresponding to the B and C domains of the reverse transcriptase gene, with reference to previously published sequences. To confirm that no viral DNA is present, another primer pair

was used for nested PCR in samples found to be negative in the first round of amplification, specifically 5'-GGATGTATCTGCGGCGTTT-3' (SEQ ID NO: 4) (nucleotides 510 to 528) and 5'-CCCAAATCAAGAAAAACAGAACA-3' (SEQ ID NO: 5) (nucleotides 953 to 931).